

Comments /
Suggestions

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Result No.	Score	% Match	Query Length	DB	ID	Description
1	425	100.0	82	9	ADZ88902	Adz88902 Human pro
2	425	100.0	85	5	AAE24393	Aae24393 Human pro
3	425	100.0	85	8	ADS75507	Ads75507 Prokineti
4	425	100.0	86	4	AAB70146	Aab70146 Human G p
5	425	100.0	86	5	ABB76801	Abb76801 Human ZAQ
6	425	100.0	86	5	ABJ05338	Abj05338 Human ZAQ
7	425	100.0	86	5	AAO15529	Aao15529 Human phy
8	425	100.0	86	5	ABB06306	Abb06306 Human G p
9	425	100.0	86	5	AAE24394	Aae24394 Human pro
10	425	100.0	86	5	AAE24383	Aae24383 Human pro
11	425	100.0	86	7	ADD69104	Add69104 Human ZAQ
12	425	100.0	86	7	ADO05360	Ado05360 Human pro
13	425	100.0	86	8	ADN43256	Adn43256 Amino aci
14	425	100.0	86	8	ADR24003	Adr24003 Human ZAQ
15	425	100.0	86	8	ADS86471	Ads86471 Human ZAQ
16	425	100.0	86	8	ADS75508	Ads75508 Prokineti
17	425	100.0	86	8	ADS75494	Ads75494 Human pro
18	425	100.0	86	8	ADS75511	Ads75511 Prokineti
19	425	100.0	86	9	ADW00759	Adw00759 Amino aci
20	425	100.0	86	9	ADZ58575	Adz58575 Human ZAQ
21	425	100.0	86	9	AEB45594	Aeb45594 Human Zve
22	425	100.0	86	9	AED00599	Aed00599 Partial h
23	425	100.0	87	5	AAE24395	Aae24395 Human pro
24	425	100.0	87	8	ADS75509	Ads75509 Prokineti
25	425	100.0	89	5	AAE24392	Aae24392 Human pro
26	425	100.0	89	8	ADS75506	Ads75506 Prokineti
27	425	100.0	105	3	AAZ66745	Aaz66745 Membrane-
28	425	100.0	105	3	AAB18453	Aab18453 A human T
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37	425	100.0	105	5	AAU83674	Aau83674 Human PRO
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ALIGNMENTS

RESULT 1

ADZ88902

ID ADZ88902 standard; protein; 82 AA.

XX

AC ADZ88902;

XX

DT 14-JUL-2005 (first entry)

Comments /
Suggestions

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http://es/ScoreAccessWeb/GetItem.action?AppId=10713567&seqId=549046&ItemName=... 7/28/2006

1	425	100.0	105	2	US-09-712-529-5	Sequence 5, Appli
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3	425	100.0	105	2	US-10-212-355-5	Sequence 5, Appli
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5	425	100.0	105	2	US-09-990-444-371	Sequence 371, App
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11	425	100.0	105	3	US-09-989-728-371	Sequence 371, App
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13	425	100.0	105	3	US-09-997-653-371	Sequence 371, App
14	425	100.0	105	3	US-09-989-293A-371	Sequence 371, App
15	413	97.2	105	2	US-09-621-976-5350	Sequence 5350, Ap
16	330	77.6	80	2	US-09-513-999C-4698	Sequence 4698, Ap
17	264	62.1	108	2	US-09-712-529-2	Sequence 2, Appli
18	264	62.1	108	2	US-10-212-201A-2	Sequence 2, Appli
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21	102	24.0	186	2	US-09-949-016-7146	Sequence 7146, Ap
22	102	24.0	207	2	US-09-161-241-13	Sequence 13, Appl
23	102	24.0	259	2	US-09-161-241-12	Sequence 12, Appl
24	102	24.0	259	2	US-09-949-016-6872	Sequence 6872, Ap
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26	102	24.0	259	2	US-10-015-389A-70	Sequence 70, Appl
27	102	24.0	259	2	US-10-006-768A-70	Sequence 70, Appl
28	102	24.0	259	2	US-10-015-671A-70	Sequence 70, Appl
29	102	24.0	259	2	US-10-015-393A-70	Sequence 70, Appl
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35	102	24.0	259	3	US-10-015-386A-70	Sequence 70, Appl
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ALIGNMENTS

RESULT 1

US-09-712-529-5

; Sequence 5, Application US/09712529

; Patent No. 6485938

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Bishop, Paul D.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Thompson, Penny P.

; TITLE OF INVENTION: Human Zven Proteins

SCORE Search Results Details for Application 10713567 and Search Result us-10-713-567-3_copy_7_77.rapbm.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 00:40:02 ; Search time 176.5 Seconds
(without alignments)
186.336 Million cell updates/sec

Title: US-10-713-567-3_COPY_7_77
Perfect score: 425
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_Main:*

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

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3	425	100.0	85	4	US-10-323-157-16	Sequence 16, Appl
4	425	100.0	85	5	US-10-713-567-16	Sequence 16, Appl
5	425	100.0	85	5	US-10-811-328-16	Sequence 16, Appl
6	425	100.0	85	5	US-10-912-907-16	Sequence 16, Appl
7	425	100.0	85	5	US-10-415-724-16	Sequence 16, Appl
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9	425	100.0	86	4	US-10-016-481-17	Sequence 17, Appl
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12	425	100.0	86	4	US-10-417-426-9	Sequence 9, Appli
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14	425	100.0	86	5	US-10-680-554-5	Sequence 5, Appli
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22	425	100.0	86	5	US-10-912-907-17	Sequence 17, Appl
23	425	100.0	86	5	US-10-415-724-3	Sequence 3, Appli
24	425	100.0	86	5	US-10-415-724-17	Sequence 17, Appl
25	425	100.0	86	5	US-10-871-152-22	Sequence 22, Appl
26	425	100.0	86	5	US-10-503-554A-82	Sequence 82, Appl
27	425	100.0	86	5	US-10-343-095A-117	Sequence 117, App
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33	425	100.0	87	5	US-10-912-907-18	Sequence 18, Appl
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45	425	100.0	105	3	US-09-989-731-371	Sequence 371, App

ALIGNMENTS

RESULT 1

US-10-977-113-11

; Sequence 11, Application US/10977113

; Publication No. US20050143287A1

; GENERAL INFORMATION:

; APPLICANT: Zhou, Qun-Yong

; TITLE OF INVENTION: Primate Prokineticin and Prokineticin

; TITLE OF INVENTION: Receptor Polypeptides, Related Compositions and Methods

; FILE REFERENCE: 66778-377

; CURRENT APPLICATION NUMBER: US/10/977,113

; CURRENT FILING DATE: 2004-10-29

Comments /
Suggestions

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5	288	67.8	80	7	US-11-304-129-34	Sequence 34, Appl
6	102	24.0	259	6	US-10-196-749-250	Sequence 250, App
7	101	23.8	272	7	US-11-197-665-4	Sequence 4, Appli
8	100.5	23.6	350	7	US-11-101-316-8	Sequence 8, Appli
9	97	22.8	266	6	US-10-505-928-533	Sequence 533, App
10	97	22.8	266	7	US-11-197-665-2	Sequence 2, Appli
11	75.5	17.8	446	7	US-11-293-697-3580	Sequence 3580, Ap
12	72.5	17.1	425	7	US-11-293-697-4381	Sequence 4381, Ap
13	67.5	15.9	909	6	US-10-449-902-44686	Sequence 44686, A
14	67	15.8	491	7	US-11-217-997-30	Sequence 30, Appl
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18	67	15.8	1547	7	US-11-217-997-22	Sequence 22, Appl
19	67	15.8	1577	7	US-11-217-997-16	Sequence 16, Appl
20	67	15.8	1577	7	US-11-217-997-20	Sequence 20, Appl
21	67	15.8	1594	7	US-11-217-997-18	Sequence 18, Appl
22	67	15.8	1620	7	US-11-217-997-42	Sequence 42, Appl
23	67	15.8	1653	7	US-11-217-997-40	Sequence 40, Appl
24	66	15.5	85	6	US-10-525-126-295	Sequence 295, App
25	65.5	15.4	92	6	US-10-449-902-41737	Sequence 41737, A
26	65	15.3	575	7	US-11-217-997-32	Sequence 32, Appl
27	65	15.3	1418	7	US-11-217-997-38	Sequence 38, Appl
28	65	15.3	1450	7	US-11-217-997-6	Sequence 6, Appli
29	64.5	15.2	342	7	US-11-038-753-1	Sequence 1, Appli
30	64.5	15.2	355	6	US-10-504-973-33	Sequence 33, Appl
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32	64.5	15.2	461	7	US-11-183-218-32	Sequence 32, Appl
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34	63	14.8	243	7	US-11-320-192-9	Sequence 9, Appli
35	62	14.6	243	7	US-11-320-192-12	Sequence 12, Appl
36	62	14.6	1198	7	US-11-217-997-14	Sequence 14, Appl
37	61.5	14.5	277	6	US-10-511-937-2455	Sequence 2455, Ap
38	61	14.4	569	6	US-10-449-902-46970	Sequence 46970, A
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45	59	13.9	713	7	US-11-175-714-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-11-304-129-21

; Sequence 21, Application US/11304129

; Publication No. US20060088915A1

; GENERAL INFORMATION:

; APPLICANT: OHTAKI, Tetsuya

; APPLICANT: MASUDA, Yasushi

; APPLICANT: TAKATSU, Yoshihiro

; APPLICANT: WATANABE, Takuya

SCORE Search Re

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OM protein - protein search, using sw model.

Run on: June 28, 2006, 00:32:53 ; Search time 24 Seconds
(without alignments)
284.641 Million cell updates/sec

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Perfect score: 425
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Match	Length			
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4	77.5	18.2	473	2	A56175	adhesive plaque pr
5	73	17.2	2531	2	T31070	notch homolog - se
6	71.5	16.8	1178	1	A39804	thrombospondin pre
7	71	16.7	112	2	I51909	colipase precursor
8	71	16.7	286	2	S34665	collagen, cuticula

9	70.5	16.6	591	2	I48141	acrogranin - guine
10	70.5	16.6	2318	2	S45306	notch 3 protein -
11	70	16.5	112	1	XLHU	colipase precursor
12	69	16.2	593	1	GYHU	granulin precursor
13	68.5	16.1	850	2	T14450	serine/threonine k
14	68.5	16.1	1172	2	A42587	thrombospondin 2 p
15	68	16.0	547	2	A33901	mannosyl-oligosacc
16	68	16.0	601	2	B36346	fibulin 1 precurs
17	68	16.0	683	2	C36346	fibulin 1 precurs
18	68	16.0	1101	2	T16840	hypothetical prote
19	68	16.0	1150	2	A41641	mannosyl-oligosacc
20	68	16.0	5147	1	IJFFTM	cadherin-related t
21	67	15.8	237	2	S45463	probable membrane
22	67	15.8	2215	2	T00348	LR11 protein - mou
23	66.5	15.6	1376	2	G00043	osteonidogen - hum
24	66	15.5	1172	1	TSHUP2	thrombospondin 2 p
25	65.5	15.4	251	2	A55035	cysteine-rich prot
26	65.5	15.4	802	2	T24293	hypothetical prote
27	65.5	15.4	949	2	T24294	hypothetical prote
28	65	15.3	112	2	A46717	colipase precursor
29	64.5	15.2	191	2	H71370	hypothetical prote
30	64.5	15.2	461	1	A35356	tumor necrosis fac
31	64.5	15.2	1574	2	T13954	MEGF6 protein - ra
32	64	15.1	117	2	H72706	hypothetical prote
33	64	15.1	217	2	A98196	hypothetical prote
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36	64	15.1	1143	2	T22952	hypothetical prote
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38	63.5	14.9	1847	2	T18308	probable vitellog
39	63	14.8	589	2	B38128	epithelin/granulin
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43	62.5	14.7	895	1	IJXLCP	EP-cadherin precu
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ALIGNMENTS

RESULT 1

JC7188

REIC protein - human

C;Species: Homo sapiens (man)

C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

C;Accession: JC7188

R;Tsugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.

Biochem. Biophys. Res. Commun. 268, 20-24, 2000

A;Title: A REIC gene shows down-regulation in human immortalized cells and human tumor

A;Reference number: JC7188; MUID:20119095; PMID:10652205

A;Accession: JC7188

A;Molecule type: mRNA

A;Residues: 1-350

A;Cross-references: UNIPARC:UPI0000179471; DDBJ:AB034203

A;Experimental source: heart

C;Comment: This protein is a secreted glycoprotein for head induction in amphibian emb

C;Genetics:

A;Gene: reic

C;Superfamily: human REIC protein

Comments /
Suggestions

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5	399	93.9	81	2	Q8K457_MOUSE	Q8k457 mus musculu
6	378	88.9	81	2	Q3ZFI2_BOVIN	Q3zfi2 bos taurus
7	306	72.0	104	2	Q2XXR8_VARVA	Q2xxr8 varanus var
8	301	70.8	104	2	Q2XXR7_VARVA	Q2xxr7 varanus var
9	288	67.8	81	1	VPRA_DENPO	P25687 dendroaspis
10	277	65.2	108	2	Q863H4_BOVIN	Q863h4 bos taurus
11	268	63.1	106	2	Q4RVU3_TETNG	Q4rvu3 tetraodon n
12	264	62.1	108	2	Q6ISR0_HUMAN	Q6isr0 homo sapien
13	259	60.9	107	1	PROK2_RAT	Q8r413 rattus norv
14	259	60.9	107	2	Q50E37_9MURI	Q50e37 arvicanthis
15	259	60.9	107	2	Q50E38_9MURI	Q50e38 arvicanthis
16	258	60.7	102	2	Q4SR12_TETNG	Q4sr12 tetraodon n
17	257	60.5	128	2	Q863H5_BOVIN	Q863h5 bos taurus
18	247.5	58.2	96	2	Q8JFQ0_BOMMX	Q8jfq0 bombina max
19	243.5	57.3	129	1	PROK2_HUMAN	Q9hc23 homo sapien
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21	242.5	57.1	96	2	Q5W280_BOMOR	Q5w280 bombina ori
22	238.5	56.1	128	1	PROK2_MOUSE	Q9qxu7 mus musculu
23	238.5	56.1	128	2	Q50E33_9MURI	Q50e33 arvicanthis
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34	161	37.9	86	2	Q50E35_9MURI	Q50e35 arvicanthis
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37	117.5	27.6	124	2	Q56R10_PENMO	Q56r10 penaeus mon
38	112	26.4	96	2	Q8UUX3_CHICK	Q8uux3 gallus gall
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42	106.5	25.1	224	2	Q3KNX0_HUMAN	Q3knx0 homo sapien
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44	102	24.0	259	1	DKK2_HUMAN	Q9ubu2 homo sapien
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ALIGNMENTS

RESULT 1

PROK1_HUMAN

ID PROK1_HUMAN STANDARD; PRT; 105 AA.

AC P58294;

DT 26-SEP-2001, integrated into UniProtKB/Swiss-Prot.

DT 26-SEP-2001, sequence version 1.

DT 21-FEB-2006, entry version 35.

DE Prokineticin-1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF) (Mambakine).

GN Name=PROK1; ORFNames=UNQ600/PRO1186;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

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7	416	100.0	81	7	ADO05356	Ado05356 Human maj
8	416	100.0	81	8	ADN43258	Adn43258 Amino aci
9	416	100.0	81	8	ADR24005	Adr24005 Human ZAQ
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12	416	100.0	81	9	ADW00755	Adw00755 Amino aci
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15	416	100.0	81	9	AEB45593	Aeb45593 Human Zve
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17	416	100.0	100	9	ADY86166	Ady86166 Human Bv8
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38	416	100.0	116	8	ADS86981	Ads86981 Human Zve
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41	404	97.1	80	9	ADZ88901	Adz88901 Mouse pro
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44	404	97.1	81	5	ABB06963	Abb06963 Rat G pro
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ALIGNMENTS

RESULT 1

ABG94400

ID ABG94400 standard; protein; 80 AA.

XX

AC ABG94400;

XX

DT 27-NOV-2002 (first entry)

SCORE Search Results Details for Application 10713567 and Search Result us-10-713-567-6_copy_7_77.rai.

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OM protein - protein search, using sw model

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Run on:      June 28, 2006, 00:39:12 ; Search time 36 Seconds
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Perfect score: 416
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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

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Post-processing: Minimum Match 0%
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7:   /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
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3	416	100.0	108	2	US-10-212-355-2	Sequence 2, Appli
4	264	63.5	105	2	US-09-712-529-5	Sequence 5, Appli
5	264	63.5	105	2	US-10-212-201A-5	Sequence 5, Appli
6	264	63.5	105	2	US-10-212-355-5	Sequence 5, Appli
7	264	63.5	105	2	US-09-991-181-371	Sequence 371, App
8	264	63.5	105	2	US-09-990-444-371	Sequence 371, App
9	264	63.5	105	2	US-09-997-333-371	Sequence 371, App
10	264	63.5	105	2	US-09-992-598-371	Sequence 371, App
11	264	63.5	105	2	US-09-989-735-371	Sequence 371, App
12	264	63.5	105	3	US-09-989-726-371	Sequence 371, App
13	264	63.5	105	3	US-09-997-514-371	Sequence 371, App
14	264	63.5	105	3	US-09-989-728-371	Sequence 371, App
15	264	63.5	105	3	US-09-997-349-371	Sequence 371, App
16	264	63.5	105	3	US-09-997-653-371	Sequence 371, App
17	264	63.5	105	3	US-09-989-293A-371	Sequence 371, App
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ALIGNMENTS

RESULT 1

US-09-712-529-2

; Sequence 2, Application US/09712529

; Patent No. 6485938

; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.

; APPLICANT: Bishop, Paul D.

; APPLICANT: Whitmore, Theodore E.

; APPLICANT: Thompson, Penny P.

; TITLE OF INVENTION: Human Zven Proteins

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6	416	100.0	81	4	US-10-467-019-19	Sequence 19, Appl
7	416	100.0	81	5	US-10-680-554-7	Sequence 7, Appli
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ALIGNMENTS

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US-10-467-019-22

; Sequence 22, Application US/10467019

; Publication No. US20040048314A1

; GENERAL INFORMATION:

; APPLICANT: Takeda Chemical Industries, Ltd.

; TITLE OF INVENTION: No. US20040048314A1el Physiological Active Peptide and Its Use

; FILE REFERENCE: P01-0295PCT

; CURRENT APPLICATION NUMBER: US/10/467,019

; CURRENT FILING DATE: 2003-08-01

; PRIOR APPLICATION NUMBER: JP2001-026820

SCORE Search Results Details for Application 10713567 and Search Result us-10-713-567-6_copy_7_77.rapbn.

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OM protein - protein search, using sw model

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Gapop 10.0 , Gapext 0.5

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	263	63.2	86	7	US-11-304-129-20	Sequence 20, Appl
5	263	63.2	105	7	US-11-304-129-22	Sequence 22, Appl
6	103	24.8	272	7	US-11-197-665-4	Sequence 4, Appli
7	100	24.0	266	6	US-10-505-928-533	Sequence 533, App
8	100	24.0	266	7	US-11-197-665-2	Sequence 2, Appli
9	97	23.3	259	6	US-10-196-749-250	Sequence 250, App
10	95	22.8	350	7	US-11-101-316-8	Sequence 8, Appli
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15	70.5	16.9	1577	7	US-11-217-997-16	Sequence 16, Appl
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17	70.5	16.9	1620	7	US-11-217-997-42	Sequence 42, Appl
18	70.5	16.9	1653	7	US-11-217-997-40	Sequence 40, Appl
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26	62.5	15.0	2026	6	US-10-505-928-831	Sequence 831, App
27	62	14.9	491	7	US-11-217-997-30	Sequence 30, Appl
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33	60.5	14.5	446	7	US-11-293-697-3580	Sequence 3580, Ap
34	60.5	14.5	1182	6	US-10-449-902-41231	Sequence 41231, A
35	60	14.4	1238	7	US-11-178-724-22	Sequence 22, Appl
36	59.5	14.3	1198	7	US-11-217-997-14	Sequence 14, Appl
37	59.5	14.3	1218	7	US-11-178-724-21	Sequence 21, Appl
38	59	14.2	1674	6	US-10-511-937-2587	Sequence 2587, Ap
39	58.5	14.1	282	6	US-10-953-349-19704	Sequence 19704, A
40	58.5	14.1	309	6	US-10-953-349-19703	Sequence 19703, A
41	58.5	14.1	335	6	US-10-953-349-19702	Sequence 19702, A
42	58.5	14.1	340	6	US-10-449-902-31539	Sequence 31539, A
43	58	13.9	102	6	US-10-953-349-26524	Sequence 26524, A
44	58	13.9	756	6	US-10-449-902-44363	Sequence 44363, A
45	57.5	13.8	97	6	US-10-196-749-468	Sequence 468, App

ALIGNMENTS

RESULT 1

US-11-304-129-34

; Sequence 34, Application US/11304129

; Publication No. US20060088915A1

; GENERAL INFORMATION:

; APPLICANT: OHTAKI, Tetsuya

; APPLICANT: MASUDA, Yasushi

; APPLICANT: TAKATSU, Yoshihiro

; APPLICANT: WATANABE, Takuya

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This page gives you Search Results detail for the Application 10713567 and Search Result us-10-7:
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OM protein - protein search, using sw model

Run on: June 28, 2006, 00:32:53 ; Search time 24 Seconds
(without alignments)
284.641 Million cell updates/sec

Title: US-10-713-567-6_COPY_7_77
Perfect score: 416
Sequence: 1 CDKDSQCGGGMCCAIVSIWVK.....TCPCLPGLACLRTSFNRFIC 71

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	95	22.8	350	2	JC7188 REIC protein - hum
2	76.5	18.4	1574	2	T13954 MEGF6 protein - ra
3	71.5	17.2	264	2	T16271 hypothetical prote
4	69.5	16.7	2471	2	A49128 cell-fate determin
5	68	16.3	313	2	S08198 cytochrome-c3 hydr
6	68	16.3	1609	1	MMHUB2 laminin gamma-1 ch
7	67	16.1	314	1	HQDVSG cytochrome-c3 hydr
8	66	15.9	3712	2	S18253 laminin alpha-1 ch

9	65.5	15.7	1620	2	T27283	hypothetical prote
10	65.5	15.7	2195	2	T34264	hypothetical prote
11	65	15.6	112	1	XLHU	colipase precursor
12	65	15.6	4135	2	T42629	tenascin-X - bovin
13	64	15.4	1955	1	AGCH	agrin precursor -
14	63.5	15.3	1687	2	T30176	EGF repeat transme
15	63	15.1	112	2	I51909	colipase precursor
16	63	15.1	1522	2	H88380	protein T22F7.3 [i
17	63	15.1	3566	1	A40701	tenascin-X precurs
18	63	15.1	13288	2	T03099	mucin, submaxillar
19	62.5	15.0	109	2	S67091	probable membrane
20	62	14.9	250	1	A49053	CD27 antigen precu
21	62	14.9	297	2	H69609	hypothetical prote
22	62	14.9	1722	2	E89753	protein F11C7.4 [i
23	61.5	14.8	203	2	H75434	hypothetical prote
24	61.5	14.8	318	2	E87929	protein T22H2.6 [i
25	61.5	14.8	345	2	T25138	hypothetical prote
26	61.5	14.8	358	2	T25137	hypothetical prote
27	61.5	14.8	686	2	JC7569	Delta-4 protein -
28	61.5	14.8	3871	2	T22812	hypothetical prote
29	61	14.7	191	2	H71370	hypothetical prote
30	61	14.7	237	2	S45463	probable membrane
31	61	14.7	1984	2	T13171	probable vitellog
32	61	14.7	2098	2	T18397	protein CTRP - mal
33	60.5	14.5	284	2	S17820	protoporphyrin IX
34	60.5	14.5	317	1	A45865	cytochrome-c3 hydr
35	60.5	14.5	589	2	B38128	epithelin/granulin
36	60.5	14.5	825	2	S55060	fertilin alpha-II
37	60.5	14.5	905	2	S55059	fertilin alpha-I -
38	60.5	14.5	1101	2	T16840	hypothetical prote
39	60.5	14.5	2318	2	S45306	notch 3 protein -
40	60	14.4	131	1	KRSHA3	keratin high-sulfu
41	60	14.4	375	1	A60004	matrix protein - m
42	60	14.4	375	1	MFNZMS	matrix protein - m
43	60	14.4	1607	1	MMMSB2	laminin gamma-1 ch
44	60	14.4	2150	2	T32497	hypothetical prote
45	59.5	14.3	372	2	A42778	agglutinin precurs

ALIGNMENTS

RESULT 1

JC7188

REIC protein - human

C;Species: Homo sapiens (man)

C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000

C;Accession: JC7188

R;Tsugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.

Biochem. Biophys. Res. Commun. 268, 20-24, 2000

A;Title: A REIC gene shows down-regulation in human immortalized cells and human tumor

A;Reference number: JC7188; MUID:20119095; PMID:10652205

A;Accession: JC7188

A;Molecule type: mRNA

A;Residues: 1-350

A;Cross-references: UNIPARC:UPI0000179471; DDBJ:AB034203

A;Experimental source: heart

C;Comment: This protein is a secreted glycoprotein for head induction in amphibian emb

C;Genetics:

A;Gene: reic

C;Superfamily: human REIC protein

SCORE Search Results Details for Application 10713567 and Search Result us-10-713-567-6_copy_7_77.rup.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 00:22:07 ; Search time 191 Seconds
(without alignments)
343.854 Million cell updates/sec

Title: US-10-713-567-6_COPY_7_77
Perfect score: 416
Sequence: 1 CDKDSQCGGGMCCAIVSIWVK.....TCPCLPGLACLRTSFNRFIC 71

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	416	100.0	108	2	Q6ISR0_HUMAN	Q6isr0 homo sapien	
2	404	97.1	107	1	PROK2_RAT	Q8r413 rattus norv	
3	404	97.1	107	2	Q50E37_9MURI	Q50e37 arvicanthis	
4	404	97.1	107	2	Q50E38_9MURI	Q50e38 arvicanthis	

5	395.5	95.1	129	1	PROK2_HUMAN	Q9hc23	homo sapien
6	395.5	95.1	129	2	Q53Z79_HUMAN	Q53z79	homo sapien
7	383.5	92.2	128	1	PROK2_MOUSE	Q9qxu7	mus musculu
8	383.5	92.2	128	2	Q50E33_9MURI	Q50e33	arvicanthis
9	383.5	92.2	128	2	Q50E34_9MURI	Q50e34	arvicanthis
10	383.5	92.2	128	2	Q6V8J7_RAT	Q6v8j7	rattus norv
11	381	91.6	108	2	Q863H4_BOVIN	Q863h4	bos taurus
12	361	86.8	128	2	Q863H5_BOVIN	Q863h5	bos taurus
13	295	70.9	104	2	Q2XXR8_VARVA	Q2xxr8	varanus var
14	291	70.0	104	2	Q2XXR7_VARVA	Q2xxr7	varanus var
15	289	69.5	81	1	VPRA_DENPO	P25687	dendroaspis
16	278	66.8	102	2	Q4SR12_TETNG	Q4sr12	tetraodon n
17	264	63.5	105	1	PROK1_HUMAN	P58294	homo sapien
18	264	63.5	105	2	Q5VWD4_HUMAN	Q5vwd4	homo sapien
19	263	63.2	105	2	Q8TC69_HUMAN	Q8tc69	homo sapien
20	259	62.3	105	1	PROK1_RAT	Q8r414	rattus norv
21	256	61.5	81	2	Q3ZFI2_BOVIN	Q3zfi2	bos taurus
22	253	60.8	81	2	Q8K457_MOUSE	Q8k457	mus musculu
23	238	57.2	86	2	Q50E35_9MURI	Q50e35	arvicanthis
24	238	57.2	86	2	Q50E36_9MURI	Q50e36	arvicanthis
25	223	53.6	82	2	Q2TBS7_BOVIN	Q2tbs7	bos taurus
26	221.5	53.2	96	1	BV8_BOMVA	Q9pw66	bombina var
27	221.5	53.2	96	2	Q8JFQ0_BOMMX	Q8jfq0	bombina max
28	217.5	52.3	96	2	Q5W280_BOMOR	Q5w280	bombina ori
29	210.5	50.6	96	2	Q8JFE6_BOMMX	Q8jfe6	bombina max
30	209.5	50.4	96	2	Q8JFX9_BOMMX	Q8jfx9	bombina max
31	209.5	50.4	96	2	Q8JFY1_BOMMX	Q8jfy1	bombina max
32	207	49.8	96	2	Q8JFY0_BOMMX	Q8jfy0	bombina max
33	202.5	48.7	96	2	Q8JFX8_BOMMX	Q8jfx8	bombina max
34	200	48.1	106	2	Q4RVU3_TETNG	Q4rvu3	tetraodon n
35	198.5	47.7	96	2	Q8JFY2_BOMMX	Q8jfy2	bombina max
36	122.5	29.4	124	2	Q56R10_PENMO	Q56r10	penaeus mon
37	111.5	26.8	221	1	DKK4_MOUSE	Q8vej3	mus musculu
38	110	26.4	96	2	Q8UUX3_CHICK	Q8uux3	gallus gall
39	105.5	25.4	256	2	Q5EHU6_GECJA	Q5ehu6	gecko japon
40	103	24.8	104	2	Q56R11_PACLE	Q56r11	pacifastacu
41	103	24.8	272	1	DKK1_MOUSE	O54908	mus musculu
42	103	24.8	272	2	Q80UL5_MOUSE	Q80ul5	m dickkopf
43	101	24.3	39	2	Q50E61_9MURI	Q50e61	arvicanthis
44	100.5	24.2	224	1	DKK4_HUMAN	Q9ubt3	homo sapien
45	100.5	24.2	224	2	Q3KNX0_HUMAN	Q3knx0	homo sapien

ALIGNMENTS

RESULT 1

Q6ISR0_HUMAN

ID Q6ISR0_HUMAN PRELIMINARY; PRT; 108 AA.

AC Q6ISR0;

DT 10-MAY-2005, integrated into UniProtKB/TrEMBL.

DT 10-MAY-2005, sequence version 1.

DT 21-FEB-2006, entry version 6.

DE Prokineticin 2.

GN Name=PROK2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.

OX NCBI_TaxID=9606;

RN [1]